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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=12; hr=15; min=24; sec=40; ms=444; ]

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Application No: 10588114 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2008-08-14 10:59:26.184  
**Finished:** 2008-08-14 10:59:29.870  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 686 ms  
**Total Warnings:** 67  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 99  
**Actual SeqID Count:** 99

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)

**Input Set:**

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**Started:** 2008-08-14 10:59:26.184  
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**Total Warnings:** 67  
**Total Errors:** 0  
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (53) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.  
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES  
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10588114  
<141> 2008-08-14

<150> PCT/US05/002633  
<151> 2005-01-28

<150> 60/628,997  
<151> 2004-11-18

<150> 60/607,684  
<151> 2004-09-07

<150> 60/557,152  
<151> 2004-03-26

<150> 60/539,774  
<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

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<220>  
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1 5

<210> 2  
<211> 37  
<212> PRT  
<213> Homo sapiens

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Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser  
1 5 10 15  
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr

20

25

30

Met Gly Leu Leu Thr  
35

<210> 3  
<211> 14  
<212> PRT  
<213> Rous sarcoma virus

<400> 3  
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg  
1 5 10

<210> 4  
<211> 25  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown: GRK6 peptide  
sequence

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Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser  
1 5 10 15  
Asp Ser Glu Glu Glu Leu Pro Thr Arg  
20 25

<210> 5  
<211> 7  
<212> PRT  
<213> Monkey virus SV40

<400> 5  
Pro Lys Lys Lys Lys Lys Val  
1 5

<210> 6  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 6  
Ala Arg Arg Arg Arg Pro  
1 5

<210> 7  
<211> 10  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown: NF kappa-B p50  
sequence

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Glu Glu Val Gln Arg Lys Arg Gln Lys Leu  
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<210> 8  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown: NF kappa-B p65  
sequence

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1 5

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<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown: Nucleoplasmin  
sequence

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Lys Lys Lys Leu Asp  
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<210> 10  
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<213> Homo sapiens

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Lys Phe Glu Arg Gln  
1 5

<210> 11  
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<400> 11

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1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly  
20 25 30

Tyr Gln Thr Ile  
35

<210> 12

<211> 35

<212> PRT

<213> Homo sapiens

<400> 12

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1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr  
20 25 30

Glu Gln Phe  
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<210> 13

<211> 27

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 13

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1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr  
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<210> 14

<211> 25

<212> PRT

<213> *Saccharomyces cerevisiae*

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Thr Leu Cys Ser Ser Arg Tyr Leu Leu  
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<210> 15

<211> 64

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 15

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1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu

20 25 30

Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala

35 40 45

Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala

50 55 60

<210> 16

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<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val

1 5 10 15

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20 25 30

Gln Gln Gln Gln Gln Arg Gly Lys Lys

35 40

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<211> 4

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: Endoplasmic

reticulum localizing sequence

<400> 17

Lys Asp Glu Leu

1

<210> 18

<211> 15

<212> PRT

<213> Human adenovirus type 19

<400> 18

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1 5 10 15

<210> 19

<211> 20

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: Interleukin-2  
sequence

<400> 19

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Val Thr Asn Ser  
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<210> 20

<211> 29

<212> PRT

<213> Homo sapiens

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu  
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr  
20 25

<210> 21

<211> 27

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Ala Leu  
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Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn  
20 25

<210> 22

<211> 18

<212> PRT

<213> Influenza A virus

<400> 22

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp  
1 5 10 15

Gln Ile

<210> 23

<211> 24  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown: Interleukin-4  
sequence

<400> 23  
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Cys Ala Gly Asn Phe Val His Gly  
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<210> 24  
<211> 37  
<212> DNA  
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<400> 24  
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<210> 25  
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<210> 26  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
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<400> 26

gccgttaatc cagattac 18

<210> 27  
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<212> DNA  
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<222> (18)..(19)  
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<212> DNA  
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<400> 28  
gaagataatg tcagggcc

18

<210> 29  
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39

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primer

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<210> 31  
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<212> DNA  
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<220>  
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<212> DNA
<213> Artificial Sequence
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<210> 35  
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<212> DNA  
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aaaggctata acggctcgcc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180  
gtcaccgttgc agcatccggaa taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
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cccgaagaac gttttccaaat gatgagcaact tttaaagtgc tgctatgtgg cgccgttata 1560  
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cttgatcggtt gggaaaccggaa actgaatgaa gcccggccca ccatggaaaaa cgcccgaaaa 1860  
ggtaaatca tgccgaacat cccgcagatg tccgctttctt ggtatggcgt gctgactgcg 1920  
gtgatcaacg cccgcagcgg tcgtcagact gtcgatgaag ccctgaaaga cgccgcagact 1980  
cgtatcacca aqtaa 1995

<210> 36  
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<212> PRT

<213> Escherichia coli

<400> 36

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20 25 30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu  
35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
325 330 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp  
340 345 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr  
355 360 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met  
370 375 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala  
385 390 395 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg  
405 410 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val  
420 425 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg  
435 440 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser  
450 455 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly  
465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu  
485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys  
500 505 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu  
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr  
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu